

TOPESD "B3ET 2360

Signal Peptide		Prodomain	
DKUZ	MSSKCAFNIVFVSIIIFIIVNGYAKDISGVKRGHERLNEIXISHYETLIMVDHEHIRASNNRARRSVTK--DQYVHLK	74	
MKUZ	MVLPITVLILLLSWAAGLGG--QYGNPKNKYIRHYEGLSYNVDSLHQAQRAKRAVSHEDQFLLLD	63	
DKUZ	FASHGRDFHLRLKRD LNTFSNKLDFYDSKGPIDVSDTHIYEGEVIGIDRNSYVFGSIHNGVFEFGKIITERDAYVVE	149	
MKUZ	FHAHGRQENLRMKRDTSLFSDEFKVTENKVLDYDTISHIYTGHIYGEEGSFHSGVIDGRFEGFKIRGGTFYIE	138	
DKUZ	HAKHYFPTNRTATITPPSTTSSATTVTKSTQPTRPLAKSNTSITAVNSKTENFIKIAESTTTSQALPEYTES	224	
MKUZ	PAERYIK-----	145	
DKUZ	SSSSSTTFPPTTEYFEDEKERNAEDELDFHSILYKESHVEDAYENVREGHVAGCGITDEVSQWMENIQNSAVEE	299	
MKUZ	-----DRIIPFHSVLYHEDDINYPHKYGPQGGCAD-----HSVFERMRKYQMTGVEE	192	
Metalloprotease Domain			
DKUZ	LPEPMKDYQKLHRKQ LHKKSAPAQQAQPPPKKYSIGDEDFKYPHQKYTKEANFAEGAFYDPSTGRRRLGSSANV	374	
MKUZ	GARAHPEKHAASSGPE LRLK-----	213	
DKUZ	ADWHQLVHERVRRATDNGAGDRGSSGGSGRGREDNKNTCSLYIQIDPLIWRHIREGIAHDRGRKYEVDEKTREE	449	
MKUZ	-----RTTLAERNTCQLYIQIDHLFFKY-----GTREA	242	
DKUZ	ITSLIAHVIJAVNYIYRNITKFDGRTEHRNIRFEVQRITKIDDSACRNSYNGPHNAFCNEHMDVSNFLNHSLEDH	524	
MKUZ	VIAQISSHVKAIDTLYQTIDESGI-----RNISFMVKRI RINTT SDEK-----PTNPFPPNIGVEKFL ELNSEG NH	310	
DKUZ	SDFCLAYVFTYRDFGTGLGLAWVASAGSAGGICEKYKITYTETVGGQYASTKRS LNTGITITFVNYNSRVPPKVS	599	
MKUZ	DDYCLAYVFIDRDFDDGLGLAWVGAPSGSSGGICEKSKLYSD-----GKKKSLNTGITITVQNYGSHVPPKVS	378	
Zn ⁺⁺			
DKUZ	QLTLAHEIGHNFGSPHDYPQECRPPGGL-----NGNYIMFASATSGDRPNNSKFSPCSI RNISNVLDVLVGN TK	667	
MKUZ	HITFAHEVGHNFGSPHDSGTETCPGESKNLGQKENGNYIMYARATSGDKLNNNKFS LCSI RNISQVLE-----KKR	449	
Disintegrin Domain			
DKUZ	RDCFKASEGAFICGNKIVESGEECDGCFNEEECKDKCCYPRLLISEYDQSLNSSAKGCTRRAKIQCSPSQGPGCLSN	742	
MKUZ	NNCFVESGQPICGNMVEQGEEDCGYSQ--CKDDCCP-----DANQPEGKKCKLKP GKQCSPSQGPGCC--TA	514	
XKUZ	-----YSDQ--CKDECCY-----DANQPEMLKCTLKPGKQCSPSQGPGCC--IT	39	
Cysteine-rich Domain			
DKUZ	SCTFIVPTSYHQKCKEETECSSHSSTCNGTIAECPEPRHRDDKIMCNHTALCIRGECSSGSPCLLNNMIKCFLTSTT	817	
MKUZ	QCAFKSKS--EKCRDSDCAKEGICNGFTALCPASDPKPNFIDCNRHITQVCINGQAGSICEKDYDLEEC--TCAS	585	
XKUZ	GCTFKRAG--ENCREESDCAKMGTCNGNSAQCPSPRENLIE--NRA TQVCIKGQCSGSICERYDLEEC--TCGS	109	
DKUZ	LPHVSKRKICDLACQDGNDISTCRSTSEFADKYNIQKGGISLQPGSPCDNFQGYCDVFLKCRAVDADGPLLRLKN	892	
MKUZ	SDGKDNKELCHVCCMKM APTSCASTGSLQWSKQSGRITITLQPGSPCNDFRGYCDVFMRCRLVDADGPLARLKK	660	
XKUZ	TDEKDDKELCHVCCMEKMIPTICASTGSEVWKAYFKGKTIILQPGSPCNEFK	161	
Transmembrane domain			
DKUZ	LLLNRKTLQTVAEWIVDNNWYLVVLMGVAFIVVMGSAFICCAVHIPSSNPKKRRARRISETLRAPMNTLRRMQRH	967	
MKUZ	AIFSPQLYENIAEWIVAHMVAVLMLGIALIMLMAGFIKICSVHIPSSNPKLPPPKPLPGTLK-----RRRPP	727	
DKUZ	NQRGAGPRSI PPPAHEAQHYSRGGDGRGGGGGGGRHGGSRSHHQAHPHDWRHQGHSIVPLPTGGSHSRNSA	1042	
MKUZ	QPIQQPPRQR PRESYQMGHMR	749	
DKUZ	ANQARRSDGRPRSTSSGRPQAIASGSGAASGAARSHGGYGAEQAIPGSIGGVQAAISSGGVVARAQLPLPLPP	1117	
DKUZ	PNGQQQQMQQQQQLLQAPPAISPQQPQAQFYTPKELPPRNKSRSSRTNNTSNTTTTNSSTAAGSGSVSGPGSG	1192	
DKUZ	AGSSSKSKSGKSAKAKDSKQSQQAANNSSSSKSKGKVPVRNIV	1239	

FIGURE 1A

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FOI 50-88874860

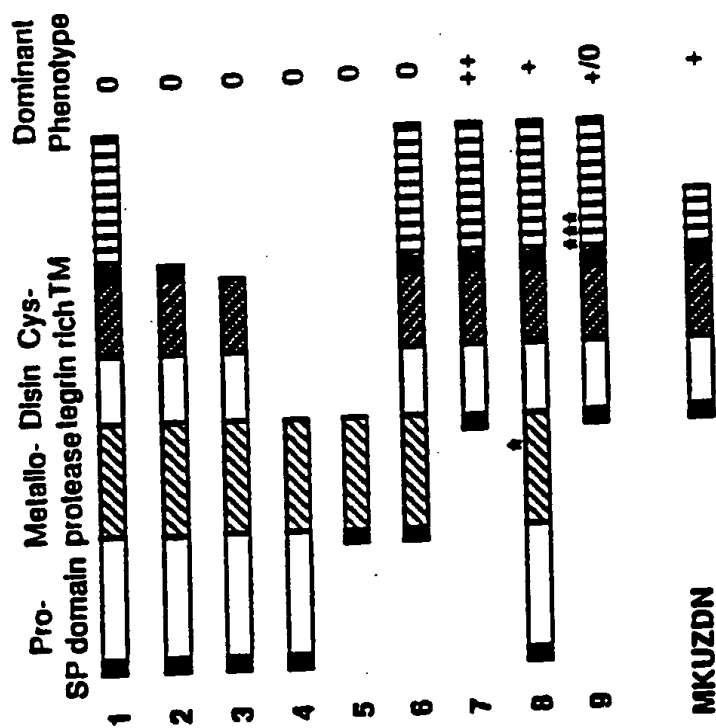


FIGURE 1 B

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

TUESDAY FEBRUARY 20 1960



FIGURE 1 C

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

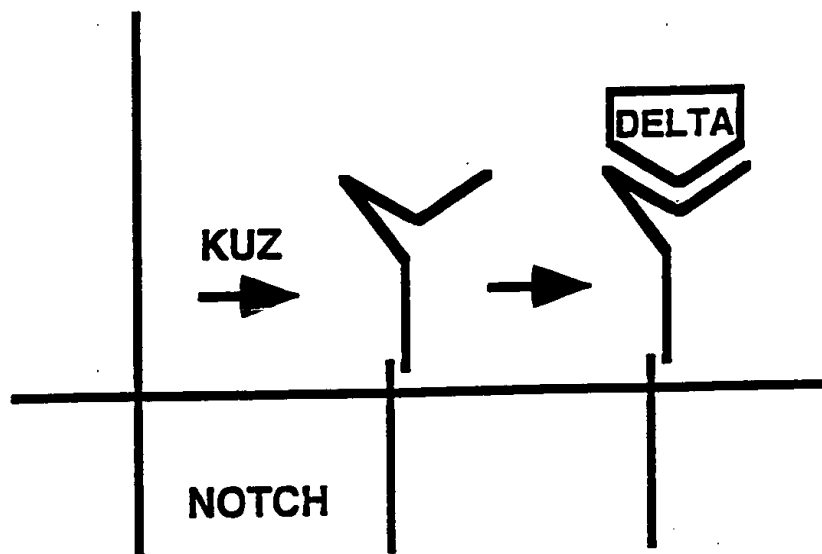


FIGURE 2

10T50" B8ET/860